

RAW SEQUENCE LISTING

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Application Serial Number: 10/511, 988
Source: PCT
Date Processed by STIC: 07/19/2005

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DATE: 07/19/2005

PATENT APPLICATION: US/10/511,988

TIME: 08:55:51

Input Set : A:\21415-0012US1.txt

Output Set: N:\CRF4\07192005\J511988.raw

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3 <110> APPLICANT: Judith A. Clements
5 <120> TITLE OF INVENTION: Method for Detecting the Presence of Risk of Prostate
6   Cancer by Detecting Products of PSA OR KLK2
8 <130> FILE REFERENCE: 21415-0012US1
10 <140> CURRENT APPLICATION NUMBER: US 10/511,988
11 <141> CURRENT FILING DATE: 2004-10-21
13 <150> PRIOR APPLICATION NUMBER: PCT/AU03/00454
14 <151> PRIOR FILING DATE: 2003-04-16
16 <150> PRIOR APPLICATION NUMBER: AU PS1870/02
17 <151> PRIOR FILING DATE: 2002-04-22
19 <160> NUMBER OF SEQ ID NOS: 43
21 <170> SOFTWARE: PatentIn version 3.2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1603
25 <212> TYPE: DNA
26 <213> ORGANISM: Human
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (38)..(577)
32 <400> SEQUENCE: 1
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34                                     Met Trp Val Pro Val Val
35                                     1           5
37 ttc ctc acc ctg tcc gtg acg tgg att ggt gct gca ccc ctc atc ctg      103
38 Phe Leu Thr Leu Ser Val Thr Trp Ile Gly Ala Ala Pro Leu Ile Leu
39          10           15           20
41 tct cgg att gtg gga ggc tgg gag tgc gag aag cat tcc caa ccc tgg      151
42 Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln Pro Trp
43          25           30           35
45 cag gtg ctt gtg gcc tct cgt ggc agg gca gtc tgc ggc ggt gtt ctg      199
46 Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly Val Leu
47          40           45           50
49 gtg cac ccc cag tgg gtc ctc aca gct gcc cac tgc atc agg aac aaa      247
50 Val His Pro Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg Asn Lys
51 55          60           65           70
53 agc gtg atc ttg ctg ggt cgg cac agc ctg ttt cat cct gaa gac aca      295
54 Ser Val Ile Leu Leu Gly Arg His Ser Leu Phe His Pro Glu Asp Thr
55          75           80           85
57 ggc cag gta ttt cag gtc agc cac agc ttc cca cac ccg ctc tac gat      343
58 Gly Gln Val Phe Gln Val Ser His Ser Phe Pro His Pro Leu Tyr Asp
59          90           95          100
61 atg agc ctc ctg aag aat cga ttc ctc agg cca ggt gat gac tcc agc      391
62 Met Ser Leu Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp Ser Ser

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63          105          110          115
65 cac gac ctc atg ctg ctc cgc ctg tca gag cct gcc gag ctc acg gat      439
66 His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu Thr Asp
67          120          125          130
69 gct gtg aag gtc atg gac ctg ccc acc cag gag cca gca ctg ggg acc      487
70 Ala Val Lys Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr
71 135          140          145          150
73 acc tgc tac gcc tca ggc tgg ggc agc att gaa cca gag gag tgt acg      535
74 Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu Cys Thr
75          155          160          165
77 cct ggg cca gat ggt gca gcc ggg agc cca gat gcc tgg gtc      577
78 Pro Gly Pro Asp Gly Ala Ala Gly Ser Pro Asp Ala Trp Val
79          170          175          180
81 tgaggggagga ggggacagga ctccctgggtc tgaggggagga gggccaagga accaggtggg      637
83 gtccagccca caacagtgtt ttgcctggc ccgtagtctt gaccccaaag aaacttcagt      697
85 gtgtggacct ccatgttatt tccaatgacg tgtgtgcgca agttcaccct cagaaggtga      757
87 ccaagttcat gctgtgtgct ggacgctgga cagggggcaa aagcacctgc tcgggtgatt      817
89 ctggggggccc acttgtctgt aatggtgtgc ttcaaggtat cacgtcatgg ggagtgaaac      877
91 catgtgccct gccgaaagg ccttcctgt acaccaaggt ggtgcattac cggaagtga      937
93 tcaaggacac catcgtggcc aaccctgag caccctatc aactccctat ttagtaaac      997
95 ttggaacctt ggaaatgacc aggccaagac tcaggcctcc ccagttctac tgaccttgt      1057
97 ccttaggtgt gaggtccagg gttgctagga aaagaaatca gcagacacag gtgtagacca      1117
99 gagtgtttct taaatggtgt aattttgtcc tctctgtgtc ctggggaata ctggccatgc      1177
101 ctggagacat atcactcaat ttctctgagg acacagatag gatgggggtgt ctgtgttatt      1237
103 tgtgggctac agagatgaaa gaggggtggg atccacactg agagagtga gagtgacatg      1297
105 tgctggacac tgtccatgaa gcaactgagca gaaagctgga ggcacaacgc accagacact      1357
107 cacagcaagg atggagctga aaacataacc cactctgtcc tggaggcact gggaagccta      1417
109 gagaaggctg tgagccaagg agggagggtc ttcccttggc atgggatggg gatgaagtaa      1477
111 ggagagggac tggacccctt ggaagctgat tcactatggg gggaggtgta ttgaagtcc      1537
113 ccagacaacc ctccagattg atgatttcc agtagaactc acagaaataa agagctgtta      1597
115 tactgg
118 <210> SEQ ID NO: 2
119 <211> LENGTH: 180
120 <212> TYPE: PRT
121 <213> ORGANISM: Human
123 <400> SEQUENCE: 2
125 Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly
126 1          5          10          15
129 Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
130          20          25          30
133 Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala
134          35          40          45
137 Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
138          50          55          60
141 His Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu
142 65          70          75          80
145 Phe His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe
146          85          90          95
149 Pro His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg

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150          100          105          110
153 Pro Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
154          115          120          125
157 Pro Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln
158          130          135          140
161 Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
162 145          150          155          160
165 Glu Pro Glu Glu Cys Thr Pro Gly Pro Asp Gly Ala Ala Gly Ser Pro
166          165          170          175
169 Asp Ala Trp Val
170          180
173 <210> SEQ ID NO: 3
174 <211> LENGTH: 492
175 <212> TYPE: DNA
176 <213> ORGANISM: Human
179 <220> FEATURE:
180 <221> NAME/KEY: CDS
181 <222> LOCATION: (1)..(489)
183 <400> SEQUENCE: 3
184 gca ccc ctc atc ctg tct cgg att gtg gga ggc tgg gag tgc gag aag      48
185 Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Lys
186 1          5          10          15
188 cat tcc caa ccc tgg cag gtg ctt gtg gcc tct cgt ggc agg gca gtc      96
189 His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val
190          20          25          30
192 tgc ggc ggt gtt ctg gtg cac ccc cag tgg gtc ctc aca gct gcc cac      144
193 Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His
194          35          40          45
196 tgc atc agg aac aaa agc gtg atc ttg ctg ggt cgg cac agc ctg ttt      192
197 Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu Phe
198          50          55          60
200 cat cct gaa gac aca ggc cag gta ttt cag gtc agc cac agc ttc cca      240
201 His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe Pro
202 65          70          75          80
204 cac ccg ctc tac gat atg agc ctc ctg aag aat cga ttc ctc agg cca      288
205 His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg Pro
206          85          90          95
208 ggt gat gac tcc agc cac gac ctc atg ctg ctc cgc ctg tca gag cct      336
209 Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro
210          100          105          110
212 gcc gag ctc acg gat gct gtg aag gtc atg gac ctg ccc acc cag gag      384
213 Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln Glu
214          115          120          125
216 cca gca ctg ggg acc acc tgc tac gcc tca ggc tgg ggc agc att gaa      432
217 Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu
218          130          135          140
220 cca gag gag tgt acg cct ggg cca gat ggt gca gcc ggg agc cca gat      480
221 Pro Glu Glu Cys Thr Pro Gly Pro Asp Gly Ala Ala Gly Ser Pro Asp
222 145          150          155          160

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224 gcc tgg gtc tga                                     492
225 Ala Trp Val
229 <210> SEQ ID NO: 4
230 <211> LENGTH: 163
231 <212> TYPE: PRT
232 <213> ORGANISM: Human
234 <400> SEQUENCE: 4
236 Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Lys
237 1 5 10 15
240 His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val
241 20 25 30
244 Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His
245 35 40 45
248 Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu Phe
249 50 55 60
252 His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe Pro
253 65 70 75 80
256 His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg Pro
257 85 90 95
260 Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro
261 100 105 110
264 Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln Glu
265 115 120 125
268 Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu
269 130 135 140
272 Pro Glu Glu Cys Thr Pro Gly Pro Asp Gly Ala Ala Gly Ser Pro Asp
273 145 150 155 160
276 Ala Trp Val
280 <210> SEQ ID NO: 5
281 <211> LENGTH: 471
282 <212> TYPE: DNA
283 <213> ORGANISM: Human
286 <220> FEATURE:
287 <221> NAME/KEY: CDS
288 <222> LOCATION: (1)..(468)
290 <400> SEQUENCE: 5
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293 1 5 10 15
295 ctt gtg gcc tct cgt ggc agg gca gtc tgc ggc ggt gtt ctg gtg cac      96
296 Leu Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly Val Leu Val His
297 20 25 30
299 ccc cag tgg gtc ctc aca gct gcc cac tgc atc agg aac aaa agc gtg      144
300 Pro Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg Asn Lys Ser Val
301 35 40 45
303 atc ttg ctg ggt cgg cac agc ctg ttt cat cct gaa gac aca ggc cag      192
304 Ile Leu Leu Gly Arg His Ser Leu Phe His Pro Glu Asp Thr Gly Gln
305 50 55 60
307 gta ttt cag gtc agc cac agc ttc cca cac ccg ctc tac gat atg agc      240

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308 Val Phe Gln Val Ser His Ser Phe Pro His Pro Leu Tyr Asp Met Ser
309 65 70 75 80
311 ctc ctg aag aat cga ttc ctc agg cca ggt gat gac tcc agc cac gac 288
312 Leu Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp Ser Ser His Asp
313 85 90 95
315 ctc atg ctg ctc cgc ctg tca gag cct gcc gag ctc acg gat gct gtg 336
316 Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu Thr Asp Ala Val
317 100 105 110
319 aag gtc atg gac ctg ccc acc cag gag cca gca ctg ggg acc acc tgc 384
320 Lys Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys
321 115 120 125
323 tac gcc tca ggc tgg ggc agc att gaa cca gag gag tgt acg cct ggg 432
324 Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Cys Thr Pro Gly
325 130 135 140
327 cca gat ggt gca gcc ggg agc cca gat gcc tgg gtc tga 471
328 Pro Asp Gly Ala Ala Gly Ser Pro Asp Ala Trp Val
329 145 150 155
332 <210> SEQ ID NO: 6
333 <211> LENGTH: 156
334 <212> TYPE: PRT
335 <213> ORGANISM: Human
337 <400> SEQUENCE: 6
339 Ile Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln Pro Trp Gln Val
340 1 5 10 15
343 Leu Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly Val Leu Val His
344 20 25 30
347 Pro Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg Asn Lys Ser Val
348 35 40 45
351 Ile Leu Leu Gly Arg His Ser Leu Phe His Pro Glu Asp Thr Gly Gln
352 50 55 60
355 Val Phe Gln Val Ser His Ser Phe Pro His Pro Leu Tyr Asp Met Ser
356 65 70 75 80
359 Leu Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp Ser Ser His Asp
360 85 90 95
363 Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu Thr Asp Ala Val
364 100 105 110
367 Lys Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys
368 115 120 125
371 Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu Cys Thr Pro Gly
372 130 135 140
375 Pro Asp Gly Ala Ala Gly Ser Pro Asp Ala Trp Val
376 145 150 155
379 <210> SEQ ID NO: 7
380 <211> LENGTH: 708
381 <212> TYPE: DNA
382 <213> ORGANISM: Human
385 <220> FEATURE:
386 <221> NAME/KEY: misc_feature
387 <222> LOCATION: (38)..(577)

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VERIFICATION SUMMARY

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